**REMARKS**

Applicants request approval of the revision to Figure 3A correcting the nucleotide at position 152 from "I" to "A". This correction is supported in the nucleotide sequence of SEQ ID NO:5 at 152. The error in Figure 3A is of a typographical nature and does not present new matter.

Applicants have added into the present specification a paper copy Sequence Listing section according to 37 C.F.R. §1.821(c) as new pages 1-4. Furthermore, attached hereto is a 3 1/2" disk containing the "Sequence Listing" in computer readable form in accordance with 37 C.F.R. §1.821(e).

The following statement is provided to meet the requirements of 37 C.F.R. §1.821(f) and 1.821(g).

I hereby state, in accordance with 37 C.F.R. §1.821(f), that the content of the attached paper and computer readable copies of the sequence listing are believed to be the same.

I hereby also state, in accordance with 37 C.F.R. §1.821(g), that the submission is not believed to include new matter.

Under U.S. rules, each sequence must be classified in <213> as an "Artificial Sequence", a sequence of "Unknown" origin, or a sequence originating in a particular organism, identified by its scientific name.

Neither the rules nor the MPEP clarify the nature of the relationship which must exist between a listed sequence

and an organism for that organism to be identified as the origin of the sequence under <213>.

Hence, counsel may choose to identify a listed sequence as associated with a particular organism even though that sequence does not occur in nature by itself in that organism (it may be, e.g., an epitopic fragment of a naturally occurring protein, or a cDNA of a naturally occurring mRNA, or even a substitution mutant of a naturally occurring sequence). Hence, the identification of an organism in <213> should not be construed as an admission that the sequence *per se* occurs in nature in said organism.

Similarly, designation of a sequence as "artificial" should not be construed as a representation that the sequence has no association with any organism. For example, a primer or probe may be designated as "artificial" even though it is necessarily complementary to some target sequence, which may occur in nature. Or an "artificial" sequence may be a substitution mutant of a natural sequence, or a chimera of two or more natural sequences, or a cDNA (i.e., intron-free sequence) corresponding to an intron-containing gene, or otherwise a fragment of a natural sequence.

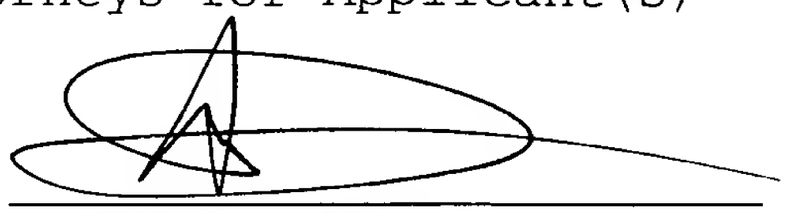
The Examiner should be able to judge the relationship of the enumerated sequences to natural sequences by giving full consideration to the specification, the art cited therein, any further art cited in an IDS, and the results of his or her sequence search against a database containing known natural sequences.

Applicants submit that the present application contains patentable subject matter and therefore urge the examiner to pass the case to issuance.

If the examiner has any questions or comments concerning the above described application, the examiner is urged to contact the undersigned at the phone number below.

Respectfully submitted,

BROWDY AND NEIMARK, P.L.L.C.
Attorneys for Applicant(s)

By 
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Telephone No.: (202) 628-5197
Facsimile No.: (202) 737-3528
F:\,C\cohn\Willner5\PTO\RESPONSE TO NOTICE TO COMPLY.doc

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1   ATG AGA GTG CTG ATT CTT TTG TGG CTG TTC ACA GCC TTT CCT GGT ATC CTG TCT GAT GTG  60
      M   R   V   L   I   L   L   W   L   F   T   A   F   P   G   I   L   S   D   V

61  CAG CTT CAG GAG TCG GGA CCT GGC CTG GTG AAG CCT TCC CAG TCT CTG TCC CTC ACC TGC 120
      Q   L   Q   E   S   G   P   G   L   V   K   P   S   Q   S   L   S   L   T   C

121 TCT GTC ACT GGT TAC TCA ATC ACC AGT GGT TAT GCC TGG AAC TGG ATC CGG CAG TTT CCA 180
      S   V   T   G   Y   S   I   T   S   G   Y   A   W   N   W   I   R   Q   F   P
                                  A

181 GGA AAC AAA CTG GAG TGG ATG GGC TAC ATA AGC TAC AGT GGT TTC ACT AGC TAC AAC CCA 240
      G   N   K   L   E   W   M   G   Y   I   S   Y   S   G   F   T   S   Y   N   P

241 TCT CTC AGA AGT CGA ATC TCT TTC ACT CGA GAC ACA TCC AAG AAC CAG TTC TTC CTG CAG 300
      S   L   R   S   R   I   S   F   T   R   D   T   S   K   N   Q   F   F   L   Q

301 TTG AAT TCT GTG ACT TCT GAG GAC ACA GCC ACA TAT TAC TGT GCA AGA TGG GAC TAC GGT 360
      L   N   S   V   T   S   E   D   T   A   T   Y   Y   C   A   R   W   D   Y   G

361 ACT ACC TAC GGG TAC TTC GAT GTC TGG GGC CAA GGG ACT ACG GTC ACC 408
      T   T   Y   G   Y   F   D   V   W   G   Q   G   T   G   V   T
                                  N3'VH   (J1)
```

FIG.3A

SEQUENCE LISTING

<110> WILLNER, Itamar
ESHHAR, Zelig

<120> DETECTION OF SMALL MOLECULES BY USE OF A PIEZOELECTRIC SENSOR

<130> WILLNER=5

<140> US 09/889,936
<141> 2001-07-25

<150> PCT/IL00/00048
<151> 2000-01-25

<150> IL 128212
<151> 1999-01-25

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<170> PatentIn version 3.1

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1               5                  10                  15

ctg tct gat gtg cag ctt cag gag tcg gga cct ggc ctg gtg aag cct        96
Leu Ser Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro
            20                  25                  30

tcc cag tct ctg tcc ctc acc tgc tct gtc act ggt tac tca atc acc       144
Ser Gln Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr
        35                  40                  45

agt ggt tat gcc tgg aac tgg atc cgg cag ttt cca gga aac aaa ctg       192
Ser Gly Tyr Ala Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu
    50                  55                  60

gag tgg atg ggc tac ata agc tac agt ggt ttc act agc tac aac cca       240
Glu Trp Met Gly Tyr Ile Ser Tyr Ser Gly Phe Thr Ser Tyr Asn Pro
65                  70                  75                  80

tct ctc aga agt cga atc tct ttc act cga gac aca tcc aag aac cag       288
Ser Leu Arg Ser Arg Ile Ser Phe Thr Arg Asp Thr Ser Lys Asn Gln
                85                  90                  95

ttc ttc ctg cag ttg aat tct gtg act tct gag gac aca gcc aca tat       336
Phe Phe Leu Gln Leu Asn Ser Val Thr Ser Glu Asp Thr Ala Thr Tyr
            100                 105                 110

tac tgt gca aga tgg gac tac ggt act acc tac ggg tac ttc gat gtc       384
Tyr Cys Ala Arg Trp Asp Tyr Gly Thr Thr Tyr Gly Tyr Phe Asp Val
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20 25 30

Ser Gln Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr
35 40 45

Ser Gly Tyr Ala Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu
50 55 60

Glu Trp Met Gly Tyr Ile Ser Tyr Ser Gly Phe Thr Ser Tyr Asn Pro
65 70 75 80

Ser Leu Arg Ser Arg Ile Ser Phe Thr Arg Asp Thr Ser Lys Asn Gln
85 90 95

Phe Phe Leu Gln Leu Asn Ser Val Thr Ser Glu Asp Thr Ala Thr Tyr
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1 5 10 15

tca gca gga gag aag gtc act atg agc tgc aag tcc agt cag agt ctg 96
Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu
20 25 30

tta aac agt aga aat caa aag aac tac ttg gcc tgg tac cag cag aaa 144
Leu Asn Ser Arg Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys
35 40 45

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cca gga cag cct cct aaa ctt ttg atc tac ggg gta ttt att agg gat      192
Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Gly Val Phe Ile Arg Asp
    50                  55                  60

tct ggg gtc cct gat cgc ttc aca ggc agt gga tct gga acc gat ttc      240
Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe
65                  70                  75                  80

act ctt acc atc agc agt gtg cag gct gaa gac ctg gca gtt tat tac      288
Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr
                85                  90                  95

tgt cag aat gat cat att tat ccg tac acg ttc gga ggg ggg acc aag      336
Cys Gln Asn Asp His Ile Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys
            100                 105                 110

ctg gaa ata aaa                                                      348
Leu Glu Ile Lys
        115
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<213> Homo sapiens

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            20                  25                  30

Leu Asn Ser Arg Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys
        35                  40                  45

Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Gly Val Phe Ile Arg Asp
    50                  55                  60

Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe
65                  70                  75                  80

Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr
                85                  90                  95

Cys Gln Asn Asp His Ile Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys
            100                 105                 110

Leu Glu Ile Lys
        115
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